



ENTERED

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/743,674

DATE: 04/03/2003

TIME: 13:27:50

Input Set : A:\EP.txt

Output Set: N:\CRF4\04032003\I743674.raw

3 <110> APPLICANT: Dlawer, Ala' Aldeen
4 Todd, Ian
6 <120> TITLE OF INVENTION: SCREENING FOR NEISSERIAL VACCINE CANDIDATES AND VACCINES
AGAINST
7 PATHOGENIC NEISSERIA
9 <130> FILE REFERENCE: 15-840
11 <140> CURRENT APPLICATION NUMBER: US 09/743,674
12 <141> CURRENT FILING DATE: 2001-01-10
14 <150> PRIOR APPLICATION NUMBER: PCT/GB99/02205
15 <151> PRIOR FILING DATE: 1999-07-09
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2761
23 <212> TYPE: DNA
24 <213> ORGANISM: Neisseria meningitidis
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (119)..(2761)
29 <223> OTHER INFORMATION:

W--> 31 <400> 1

32	gattgatgca aatatgcaca gatgtttttg aaaaaagatg gagatatgtc ataatttgta	60
34	aaaacggcga atgattgccg tttaaaatgt ggcgcggtc ggtacattca catattaa	118
36	atg-eee-gcc-ggc-cga-ctg-ccc-cgc-cga-tgc-ccg-atg-atg-acg-aaa-ttt	166
37	Met Pro Ala Gly Arg Leu Pro Arg Arg Cys Pro Met Met Thr Lys Phe	
38	1 5 10 15	
40	aca gac tgt acg cgg tca aac cgt att cag ccg cca acc cac agg gga	214
41	Thr Asp Cys Thr Arg Ser Asn Arg Ile Gln Pro Pro Thr His Arg Gly	
42	20 25 30	
44	tac atc ttg aaa aac aac aga caa atc aaa ctg att gcc gcc tcc gtc	262
45	Tyr Ile Leu Lys Asn Asn Arg Gln Ile Lys Leu Ile Ala Ala Ser Val	
46	35 40 45	
48	gca gtt gcc gca tcc ttt cag gca cat gct gga ctg ggc gga ctg aat	310
49	Ala Val Ala Ala Ser Phe Gln Ala His Ala Gly Leu Gly Gly Leu Asn	
50	50 55 60	
52	atc cag tcc aac ctt gac gaa ccc ttt tcc ggc agc att acc gta acc	358
53	Ile Gln Ser Asn Leu Asp Glu Pro Phe Ser Gly Ser Ile Thr Val Thr	
54	65 70 75 80	
56	ggc gaa gaa gcc aaa gcc ctg cta ggc ggc ggc agc gtt acc gtt tcc	406
57	Gly Glu Glu Ala Lys Ala Leu Leu Gly Gly Gly Ser Val Thr Val Ser	
58	85 90 95	
60	gaa aaa ggc ctg acc gcc aaa gtc cac aag ttg ggc gac aaa gcc gtc	454
61	Glu Lys Gly Leu Thr Ala Lys Val His Lys Leu Gly Asp Lys Ala Val	
62	100 105 110	

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64	att gcc gtt tct tcc gaa cag gca gtc cgc gat ccc gtc ctg gta ttc	502
65	Ile Ala Val Ser Ser Glu Gln Ala Val Arg Asp Pro Val Leu Val Phe	
66	115 120 125	
68	cgc atc ggc gca ggc gca cag gta cgc gaa tac acc gcc atc ctc gat	550
69	Arg Ile Gly Ala Gly Ala Gln Val Arg Glu Tyr Thr Ala Ile Leu Asp	
70	130 135 140	
72	cct gtc ggc tac tcg ccc aaa acc aaa tct gca ctt tca gac ggc aag	598
73	Pro Val Gly Tyr Ser Pro Lys Thr Lys Ser Ala Leu Ser Asp Gly Lys	
74	145 150 155 160	
76	aca cac cgc aaa acc gct ccg aca gca gag tcc caa gaa aat caa aac	646
77	Thr His Arg Lys Thr Ala Pro Thr Ala Glu Ser Gln Glu Asn Gln Asn	
78	165 170 175	
80	gcc aaa gcc ctc cgc aaa acc gat aaa aaa gac agc gcg aac gca gcc	694
81	Ala Lys Ala Leu Arg Lys Thr Asp Lys Lys Asp Ser Ala Asn Ala Ala	
82	180 185 190	
84	gtc aaa ccg gcg tac aac ggc aaa acc cat acc gtc cgc aaa ggc gaa	742
85	Val Lys Pro Ala Tyr Asn Gly Lys Thr His Thr Val Arg Lys Gly Glu	
86	195 200 205	
88	acg gtc aaa cag att gcc gcc gcc atc cgc ccg aaa cac ctg acg ctc	790
89	Thr Val Lys Gln Ile Ala Ala Ala Ile Arg Pro Lys His Leu Thr Leu	
90	210 215 220	
92	gaa cag gtt gcc gat gcg ctg ctg aag gca aac cca aat gtt tcc gca	838
93	Glu Gln Val Ala Asp Ala Leu Leu Lys Ala Asn Pro Asn Val Ser Ala	
94	225 230 235 240	
96	cac ggc aga ctg cgt gcg ggc agc gtg ctt cac att ccg aat ctg aac	886
97	His Gly Arg Leu Arg Ala Gly Ser Val Leu His Ile Pro Asn Leu Asn	
98	245 250 255	
100	agg atc aaa gcg gaa caa ccc aaa ccg caa acg gcg aaa ccc aaa gcc	934
101	Arg Ile Lys Ala Glu Gln Pro Lys Pro Gln Thr Ala Lys Pro Lys Ala	
102	260 265 270	
104	gaa acc gca tcc atg ccg tcc gaa ccg tcc aaa cag gca acg gta gag	982
105	Glu Thr Ala Ser Met Pro Ser Glu Pro Ser Lys Gln Ala Thr Val Glu	
106	275 280 285	
108	aaa ccg gtt gaa aaa cct gaa gca aaa gtt gcc gcg ccc gaa gca aaa	1030
109	Lys Pro Val Glu Lys Pro Glu Ala Lys Val Ala Ala Pro Glu Ala Lys	
110	290 295 300	
112	gcg gaa aaa ccg gcc gtt cga ccc gaa cct gta ccc gct gca aat act	1078
113	Ala Glu Lys Pro Ala Val Arg Pro Glu Pro Val Pro Ala Ala Asn Thr	
114	305 310 315 320	
116	gcc gca tcg gaa acc gct gcc gaa tcc gcc ccc caa gaa gcc gcc gct	1126
117	Ala Ala Ser Glu Thr Ala Ala Glu Ser Ala Pro Gln Glu Ala Ala Ala	
118	325 330 335	
120	tct gcc atc gac acg ccg acc gac gaa acc ggt aac gcc gtt tcc gaa	1174
121	Ser Ala Ile Asp Thr Pro Thr Asp Glu Thr Gly Asn Ala Val Ser Glu	
122	340 345 350	
124	cct gtc gaa cag gtt tct gcc gaa gaa gaa acc gaa agc gga ctg ttc	1222
125	Pro Val Glu Gln Val Ser Ala Glu Glu Glu Thr Glu Ser Gly Leu Phe	
126	355 360 365	
128	ggc ggt tcg tac acc ttg ctg ctt gcc ggc gga ggc gcg gca ttg atc	1270

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129	Gly	Gly	Ser	Tyr	Thr	Leu	Leu	Leu	Ala	Gly	Gly	Gly	Ala	Ala	Leu	Ile	
130		370					375					380					
132	gcc	ctg	ctg	ctg	ctt	ttg	cgc	ctt	gcc	caa	tcc	aaa	cgc	gcg	cgc	cgt	1316
133	Ala	Leu	Leu	Leu	Leu	Leu	Arg	Leu	Ala	Gln	Ser	Lys	Arg	Ala	Arg	Arg	
134	385					390					395					400	
136	acc	gaa	gaa	tcc	gtc	cct	gag	gaa	gag	cct	gac	ctt	gac	gac	gcg	gca	1366
137	Thr	Glu	Glu	Ser	Val	Pro	Glu	Glu	Glu	Pro	Asp	Leu	Asp	Asp	Ala	Ala	
138					405					410					415		
140	gac	gac	ggc	ata	gaa	atc	acc	ttt	gcc	gaa	gtc	gaa	act	ccg	gca	acg	1414
141	Asp	Asp	Gly	Ile	Glu	Ile	Thr	Phe	Ala	Glu	Val	Glu	Thr	Pro	Ala	Thr	
142				420					425					430			
144	ccc	gaa	ccc	gct	ccg	aaa	aac	gat	gta	aac	gac	aca	ctt	gcc	tta	gat	1462
145	Pro	Glu	Pro	Ala	Pro	Lys	Asn	Asp	Val	Asn	Asp	Thr	Leu	Ala	Leu	Asp	
146			435					440					445				
148	ggg	gaa	tct	gaa	gaa	gag	ttg	tcg	gca	aaa	caa	acg	ttc	gat	gtc	gaa	1510
149	Gly	Glu	Ser	Glu	Glu	Glu	Leu	Ser	Ala	Lys	Gln	Thr	Phe	Asp	Val	Glu	
150		450				455					460						
152	acc	gat	acg	cct	tcc	aac	cgc	atc	gac	ttg	gat	ttc	gac	agc	ctg	gca	1558
153	Thr	Asp	Thr	Pro	Ser	Asn	Arg	Ile	Asp	Leu	Asp	Phe	Asp	Ser	Leu	Ala	
154	465				470					475					480		
156	gcc	gcg	caa	aac	ggc	att	tta	tcc	ggc	gca	ctt	acg	cag	gat	gaa	gaa	1606
157	Ala	Ala	Gln	Asn	Gly	Ile	Leu	Ser	Gly	Ala	Leu	Thr	Gln	Asp	Glu	Glu	
158				485					490					495			
160	acc	caa	aaa	cgc	gcg	gat	gcc	gat	tgg	aac	gcc	atc	gaa	tcc	aca	gac	1654
161	Thr	Gln	Lys	Arg	Ala	Asp	Ala	Asp	Trp	Asn	Ala	Ile	Glu	Ser	Thr	Asp	
162			500						505					510			
164	agc	gtg	tac	gag	ccc	gag	acc	ttc	aac	ccg	tac	aac	cct	gtc	gaa	atc	1702
165	Ser	Val	Tyr	Glu	Pro	Glu	Thr	Phe	Asn	Pro	Tyr	Asn	Pro	Val	Glu	Ile	
166			515				520					525					
168	gtc	atc	gac	acg	ccc	gaa	ccg	gaa	tct	gtc	gcc	caa	act	gcc	gaa	aac	1750
169	Val	Ile	Asp	Thr	Pro	Glu	Pro	Glu	Ser	Val	Ala	Gln	Thr	Ala	Glu	Asn	
170		530				535					540						
172	aaa	ccg	gaa	acc	gtc	gat	acc	gat	ttc	tcc	gac	aac	ctg	ccc	tca	aac	1798
173	Lys	Pro	Glu	Thr	Val	Asp	Thr	Asp	Phe	Ser	Asp	Asn	Leu	Pro	Ser	Asn	
174	545				550					555				560			
176	aac	cat	atc	ggc	aca	gaa	gaa	aca	gct	tcc	gca	aaa	cct	gcc	tca	ccc	1846
177	Asn	His	Ile	Gly	Thr	Glu	Glu	Thr	Ala	Ser	Ala	Lys	Pro	Ala	Ser	Pro	
178				565					570					575			
180	tcc	gga	ctg	gca	ggc	ttc	ctg	aag	gct	tcc	tcg	ccc	gaa	acc	atc	ttg	1894
181	Ser	Gly	Leu	Ala	Gly	Phe	Leu	Lys	Ala	Ser	Ser	Pro	Glu	Thr	Ile	Leu	
182			580						585					590			
184	gaa	aaa	aca	gtt	gcc	gaa	gtc	caa	aca	ccg	gaa	gag	ttg	cac	gat	ttc	1942
185	Glu	Lys	Thr	Val	Ala	Glu	Val	Gln	Thr	Pro	Glu	Glu	Leu	His	Asp	Phe	
186			595				600					605					
188	ctg	aaa	gtg	tac	gaa	acc	gat	gcc	gtc	gcg	gaa	act	gcg	cct	gaa	acg	1990
189	Leu	Lys	Val	Tyr	Glu	Thr	Asp	Ala	Val	Ala	Glu	Thr	Ala	Pro	Glu	Thr	
190		610				615					620						
192	ccc	gat	ttc	aac	gcc	gcc	gca	gac	gat	ttg	tcc	gca	ttg	ctt	caa	cct	2038
193	Pro	Asp	Phe	Asn	Ala	Ala	Ala	Asp	Asp	Leu	Ser	Ala	Leu	Leu	Gln	Pro	

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194	625	630	635	640	
196	gcc gaa gca ccg tcc gtt gag gaa aat ata acg gaa acc gtt gcc gaa	2086			
197	Ala Glu Ala Pro Ser Val Glu Glu Asn Ile Thr Glu Thr Val Ala Glu				
198	645	650	655		
200	aca ccc gac ttc aac gcc acc gca gac gat ttg tcc gca tta ctt caa	2134			
201	Thr Pro Asp Phe Asn Ala Thr Ala Asp Asp Leu Ser Ala Leu Leu Gln				
202	660	665	670		
204	cct tct gaa gta cct gcc gtt gag gaa aat gca gcg gaa atc gtt gcc	2182			
205	Pro Ser Glu Val Pro Ala Val Glu Glu Asn Ala Ala Glu Ile Val Ala				
206	675	680	685		
208	gat gat ttg tcc gca ctg ttg caa cct gct gaa gca ccg gct gtt gag	2230			
209	Asp Asp Leu Ser Ala Leu Leu Gln Pro Ala Glu Ala Pro Ala Val Glu				
210	690	695	700		
212	gaa aat gta acg gaa act gtt gcc gaa acg tcc gac ttc cac acc gcc	2278			
213	Glu Asn Val Thr Glu Thr Val Ala Glu Thr Ser Asp Phe His Thr Ala				
214	705	710	715	720	
216	gca gac gat ttg tcc gca ctg ttg caa cct gct gaa gta ccg gcc gtt	2326			
217	Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro Ala Glu Val Pro Ala Val				
218	725	730	735		
220	gag gaa aat gta acg aaa acc gtt gcc gaa ata cct gat ttc aac gcc	2374			
221	Glu Glu Asn Val Thr Lys Thr Val Ala Glu Ile Pro Asp Phe Asn Ala				
222	740	745	750		
224	acc gca gac gat ttg tcc gca tta ctt caa cct tct gaa gta ccg gcc	2422			
225	Thr Ala Asp Asp Leu Ser Ala Leu Leu Gln Pro Ser Glu Val Pro Ala				
226	755	760	765		
228	gtt gag gaa aat gca gcg gaa atc act ttg gaa acg cct gat tcc aac	2470			
229	Val Glu Glu Asn Ala Ala Glu Ile Thr Leu Glu Thr Pro Asp Ser Asn				
230	770	775	780		
232	acc tct gag gca gac gct ttg ccc gac ttc ctg aaa gac ggc gag gag	2518			
233	Thr Ser Glu Ala Asp Ala Leu Pro Asp Phe Leu Lys Asp Gly Glu Glu				
234	785	790	795	800	
236	gaa acg gta gat tgg agc atc tac ctc tcg gaa gaa aat atc cca aat	2566			
237	Glu Thr Val Asp Trp Ser Ile Tyr Leu Ser Glu Glu Asn Ile Pro Asn				
238	805	810	815		
240	aat gca gat acc agt ttc cct tcg gaa tct gta ggt tct gac gcg cct	2614			
241	Asn Ala Asp Thr Ser Phe Pro Ser Glu Ser Val Gly Ser Asp Ala Pro				
242	820	825	830		
244	tcc gaa gcg aaa tac gac ctt gcc gaa atg tat ctc gaa atc ggc gac	2662			
245	Ser Glu Ala Lys Tyr Asp Leu Ala Glu Met Tyr Leu Glu Ile Gly Asp				
246	835	840	845		
248	cgc gat gcc gct gcc gag aca gtg cag aaa ttg ctg gaa gaa gcg gaa	2710			
249	Arg Asp Ala Ala Ala Glu Thr Val Gln Lys Leu Leu Glu Glu Ala Glu				
250	850	855	860		
252	ggc gac gta ctc aaa cgt gcc caa gca ttg gcg cag gaa ttg ggt att	2758			
253	Gly Asp Val Leu Lys Arg Ala Gln Ala Leu Ala Gln Glu Leu Gly Ile				
254	865	870	875	880	
256	tga				2761
259	<210> SEQ ID NO: 2				
260	<211> LENGTH: 880				

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261 <212> TYPE: PRT

262 <213> ORGANISM: Neisseria meningitidis

264 <400> SEQUENCE: 2

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270 Thr Asp Cys Thr Arg Ser Asn Arg Ile Gln Pro Pro Thr His Arg Gly
271 20 25 30
274 Tyr Ile Leu Lys Asn Asn Arg Gln Ile Lys Leu Ile Ala Ala Ser Val
275 35 40 45
278 Ala Val Ala Ala Ser Phe Gln Ala His Ala Gly Leu Gly Gly Leu Asn
279 50 55 60
282 Ile Gln Ser Asn Leu Asp Glu Pro Phe Ser Gly Ser Ile Thr Val Thr
283 65 70 75 80
286 Gly Glu Glu Ala Lys Ala Leu Leu Gly Gly Gly Ser Val Thr Val Ser
287 85 90 95
290 Glu Lys Gly Leu Thr Ala Lys Val His Lys Leu Gly Asp Lys Ala Val
291 100 105 110
294 Ile Ala Val Ser Ser Glu Gln Ala Val Arg Asp Pro Val Leu Val Phe
295 115 120 125
298 Arg Ile Gly Ala Gly Ala Gln Val Arg Glu Tyr Thr Ala Ile Leu Asp
299 130 135 140
302 Pro Val Gly Tyr Ser Pro Lys Thr Lys Ser Ala Leu Ser Asp Gly Lys
303 145 150 155 160
306 Thr His Arg Lys Thr Ala Pro Thr Ala Glu Ser Gln Glu Asn Gln Asn
307 165 170 175
310 Ala Lys Ala Leu Arg Lys Thr Asp Lys Lys Asp Ser Ala Asn Ala Ala
311 180 185 190
314 Val Lys Pro Ala Tyr Asn Gly Lys Thr His Thr Val Arg Lys Gly Glu
315 195 200 205
318 Thr Val Lys Gln Ile Ala Ala Ala Ile Arg Pro Lys His Leu Thr Leu
319 210 215 220
322 Glu Gln Val Ala Asp Ala Leu Leu Lys Ala Asn Pro Asn Val Ser Ala
323 225 230 235 240
326 His Gly Arg Leu Arg Ala Gly Ser Val Leu His Ile Pro Asn Leu Asn
327 245 250 255
330 Arg Ile Lys Ala Glu Gln Pro Lys Pro Gln Thr Ala Lys Pro Lys Ala
331 260 265 270
334 Glu Thr Ala Ser Met Pro Ser Glu Pro Ser Lys Gln Ala Thr Val Glu
335 275 280 285
338 Lys Pro Val Glu Lys Pro Glu Ala Lys Val Ala Ala Pro Glu Ala Lys
339 290 295 300
342 Ala Glu Lys Pro Ala Val Arg Pro Glu Pro Val Pro Ala Ala Asn Thr
343 305 310 315 320
346 Ala Ala Ser Glu Thr Ala Ala Glu Ser Ala Pro Gln Glu Ala Ala Ala
347 325 330 335
350 Ser Ala Ile Asp Thr Pro Thr Asp Glu Thr Gly Asn Ala Val Ser Glu
351 340 345 350
354 Pro Val Glu Gln Val Ser Ala Glu Glu Glu Thr Glu Ser Gly Leu Phe
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VERIFICATION SUMMARY

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Output Set: N:\CRF4\04032003\I743674.raw

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L:496 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:494